**GatorSeq Data Analysis Pipeline Log**

**Version 1.0**

Went Live – January 7th, 2017

**Version 1.1**

commit cc3f1f45a96ea4172e867944969cfb06ab1726a4

Author: ServiceAccount Chamala <path-svc-mol@gator4.ufhpc>

Date:   Thu Jan 12 15:21:10 2017 -0500

* fixed bedtools coverage memory issue
* modified metrics.sh file such that all the programs are run in snakemake
* modified absolute paths to relative paths in snakemake file and config files

**Version 1.2**

commit 0cd269c12ec1fc94e6c4fec84be388c773e841a9

Author: ServiceAccount Chamala <path-svc-mol@i21b-s1.ufhpc>

Date:   Tue Feb 7 11:55:59 2017 -0500

* Reformatted metrics file to represent same as Illumina output with \*.summary.csv extension
* Added probe coverage file with same formatting as Illumina with \*.coverage.csv extension
* Above two file formats were made to accommodate data pullup from GenomeOncology
* Added code to take of sync issue in mac, where sometimes local mount of hpc does not refresh properly
* Added code to take of sync issue in mac, where sometimes local mount of hpc does not refresh
* No core analysis steps had been changed
* Reports version numbering in Start file

**Version 1.3**

commit de7f37c787accc6b3b7076e7010d846d2e6cd35a

Author: ServiceAccount Chamala <path-svc-mol@dev2.ufhpc>

Date:   Tue Aug 8 19:17:48 2017 -0400

* Added GatorseqV2\_117\_GenePanel target and probe .bed files; which includes previous 76 gene panel regions.
* "hpc\_gatorseq.config.yaml" was modified to reflect GatorseqV2\_117\_GenePanel .bed files
* No changes were made to core code.

**Version 2.0**

commit a49d42e43fc8943794594aa16972ef797d0bc07d

Author: ServiceAccount Chamala <path-svc-mol@dev2.ufhpc>

Date:   Fri Apr 13 17:16:04 2018 -0400

* Changed workflow manager from Snakemake to Nextflow
* Modularized and optimized the file paths

**Version 2.1**

commit 7dceb4fba471b757cc1f69bcbd85f4ba106ea8f9

Author: ServiceAccount Chamala <srikarchamala@gmail.com>

Date:   Tue Aug 21 21:14:57 2018 -0400

* Added translocation pipeline

**Version 3.0**

commit 514679eccc6a13cbbf685e584065b86b7d39835a

Author: ServiceAccount Chamala <srikarchamala@gmail.com>

Date:   Mon Jan 28 20:38:30 2019 -0500

* Updated gene panel to 179 genes

**Version 4.1**

commit xxxxxxxxx

Author: ServiceAccount Chamala <srikarchamala@gmail.com>

Date:   xxxxxxxxxx

* Updated 179 gene panel with additional PGx and MSI regions
* Containerized whole nextflow pipeline using docker and singularity
* Now pipeline is run directly downloading from GIT hub repository
* Changes the folder structure relative to $HOME to make portability easy
* Updated all the bioinformatics software to latest